WEST Search History

DATE: Thursday, October 24, 2002

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L18	L16 and tryptophany$	0	L18
L17	L16 and tryphophany$	0	L17
L16	l1 and l12	4	L16
L15	Tryptophany$ and l14	0	L15
L14	l1 and L13	2	L14
L13	((514/2)!.CCLS.)	4618	L13
L12	((530/350)!.CCLS.)	8398	L12
L11	L10	1	L11
L10	l2 and therapeu$	1	L10
L9	l2 and pharmaceut$	3	L9
L8	L7 and pharmac$	1	L8
L7	6221640.pn.	2	L7
L6	L5 and pharmaceu$	1	L6
L5	Rossmann AND l4	1	L5
L4	("Tryptophanyl-tRNA" OR TrpRS).clm.	9	L4
L3	L1 and l2	2	L3
L2	("Tryptophanyl-tRNA" OR TrpRS).ab.	18	L2
L1	(Schimmel-P$ or Wakasugi-K$).in.	235	L1

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#30	Search **#23 AND 46**	11:28:57	5
#27	Search **#23 AND elastase**	11:26:37	7
#24	Search **#23 AND "amino-termin*"**	11:23:05	7
#23	Search **tryptophanyl-tRNA** Field: **All Fields,** Limits: **Publication Date to 2001**	11:22:07	255
#18	Search **#17 AND human**	11:14:15	40
#17	Search **"tryptophanyl-tRNA"** Field: **Title,** Limits: **Publication Date to 2001**	11:10:24	176
#14	**Related Articles** for **PubMed** (Select **9108248**)	11:07:00	176
#9	Search **#8 AND (fragment OR derivative OR "cleavage product" OR mutant)**	10:47:19	20
#8	Search **#7 AND (human OR mammal*)**	10:45:59	205
#7	Search **tryptophany* OR TrpRS** Field: **All Fields,** Limits: **Publication Date to 2001**	10:45:32	820
#6	**Related Articles** for **PubMed** (Select **8555191**)	10:43:47	300
#4	Search **sever s** Field: **Author,** Limits: **Publication Date from 1996 to 1996**	10:35:16	2
#3	Search **losodo** Field: **Author,** Limits: **Publication Date from 1998 to 1998**	09:29:27	0
#2	Search **losodo d** Field: **Author,** Limits: **Publication Date from 1998 to 1998**	09:29:08	0
#1	Search **losodo d** Field: **All Fields,** Limits: **Publication Date from 1998 to 1998**	09:28:48	27666

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NEWS 4	Apr 09	ZDB will be removed from STN
NEWS 5	Apr 19	US Patent Applications available in IFICDB, IFIPAT, and IFIUDB
NEWS 6	Apr 22	Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
NEWS 7	Apr 22	BIOSIS Gene Names now available in TOXCENTER
NEWS 8	Apr 22	Federal Research in Progress (FEDRIP) now available
NEWS 9	Jun 03	New e-mail delivery for search results now available
NEWS 10	Jun 10	MEDLINE Reload
NEWS 11	Jun 10	PCTFULL has been reloaded
NEWS 12	Jul 02	FOREGE no longer contains STANDARDS file segment
NEWS 13	Jul 22	USAN to be reloaded July 28, 2002; saved answer sets no longer valid
NEWS 14	Jul 29	Enhanced polymer searching in REGISTRY
NEWS 15	Jul 30	NETFIRST to be removed from STN
NEWS 16	Aug 08	CANCERLIT reload
NEWS 17	Aug 08	PHARMAMarketLetter(PHARMAML) - new on STN
NEWS 18	Aug 08	NTIS has been reloaded and enhanced
NEWS 19	Aug 19	Aquatic Toxicity Information Retrieval (AQUIRE) now available on STN
NEWS 20	Aug 19	IFIPAT, IFICDB, and IFIUDB have been reloaded
NEWS 21	Aug 19	The MEDLINE file segment of TOXCENTER has been reloaded
NEWS 22	Aug 26	Sequence searching in REGISTRY enhanced
NEWS 23	Sep 03	JAPIO has been reloaded and enhanced
NEWS 24	Sep 16	Experimental properties added to the REGISTRY file
NEWS 25	Sep 16	Indexing added to some pre-1967 records in CA/CAPLUS
NEWS 26	Sep 16	CA Section Thesaurus available in CAPLUS and CA
NEWS 27	Oct 01	CASREACT Enriched with Reactions from 1907 to 1985
NEWS 28	Oct 21	EVENTLINE has been reloaded

NEWS EXPRESS	October 14 CURRENT WINDOWS VERSION IS V6.01, CURRENT MACINTOSH VERSION IS V6.0a(ENG) AND V6.0Ja(JP), AND CURRENT DISCOVER FILE IS DATED 01 OCTOBER 2002
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FILE 'MEDLINE' ENTERED AT 10:22:58 ON 24 OCT 2002

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=> s (schimmel-p? or wakasugi-k?)/au
L1 1460 (SCHIMMEL-P? OR WAKASUGI-K?)/AU

=> s l1 and tRNA
L2 730 L1 AND TRNA

=> s l2 and synthetase
L3 644 L2 AND SYNTHETASE

=> s l3 and Rossmann
L4 1 L3 AND ROSSMANN

=> d ibib abs l4

L4 ANSWER 1 OF 1 MEDLINE
ACCESSION NUMBER: 1998221234 MEDLINE
DOCUMENT NUMBER: 98221234 PubMed ID: 9554847
TITLE: Enzyme structure with two catalytic sites for double-sieve selection of substrate.
COMMENT: Comment in: Science. 1998 Apr 24;280(5363):541
Comment in: Science. 1998 Dec 11;282(5396):1955
Comment in: Science. 1999 Jan 22;283(5401):459
AUTHOR: Nureki O; Vassylyev D G; Tateno M; Shimada A; Nakama T; Fukai S; Konno M; Hendrickson T L; **Schimmel P**; Yokoyama S
CORPORATE SOURCE: Department of Biophysics and Biochemistry, Graduate School of Science, University of Tokyo, 7-3-1 Hongo, Bunkyo-ku, Tokyo 113, Japan.
CONTRACT NUMBER: GM15539 (NIGMS)
SOURCE: SCIENCE, (1998 Apr 24) 280 (5363) 578-82.

Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: PDB-1ILE
ENTRY MONTH: 199805
ENTRY DATE: Entered STN: 19980514
Last Updated on STN: 20000303
Entered Medline: 19980507

AB High-fidelity transfers of genetic information in the central dogma can be achieved by a reaction called editing. The crystal structure of an enzyme with editing activity in translation is presented here at 2.5 angstroms resolution. The enzyme, isoleucyl-transfer RNA **synthetase**, activates not only the cognate substrate L-isoleucine but also the minimally distinct L-valine in the first, aminoacylation step. Then, in a second, "editing" step, the **synthetase** itself rapidly hydrolyzes only the valylated products. For this two-step substrate selection, a "double-sieve" mechanism has already been proposed. The present crystal structures of the **synthetase** in complexes with L-isoleucine and L-valine demonstrate that the first sieve is on the aminoacylation domain containing the **Rossmann** fold, whereas the second, editing sieve exists on a globular beta-barrel domain that protrudes from the aminoacylation domain.

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(FILE 'HOME' ENTERED AT 10:22:26 ON 24 OCT 2002)

FILE 'MEDLINE, CANCERLIT, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 10:22:58 ON 24 OCT 2002
L1 1460 S (SCHIMMEL-P? OR WAKASUGI-K?)/AU
L2 730 S L1 AND TRNA
L3 644 S L2 AND SYNTHETASE
L4 1 S L3 AND ROSSMANN

=> s l1 and tryptophanyl?
L5 17 L1 AND TRYPTOPHANYL?

=> dup rem l5
PROCESSING COMPLETED FOR L5
L6 6 DUP REM L5 (11 DUPLICATES REMOVED)

=> d ibib abs 1-6

L6 ANSWER 1 OF 6 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002056934 MEDLINE
DOCUMENT NUMBER: 21642695 PubMed ID: 11773625
TITLE: A fragment of human TrpRS as a potent antagonist of ocular angiogenesis.
AUTHOR: Otani Atsushi; Slike Bonnie M; Dorrell Michael I; Hood John; Kinder Karen; Ewalt Karla L; Cheresh David; **Schimmel Paul**; Friedlander Martin
CORPORATE SOURCE: Department of Cell Biology, The Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA 92037, USA.
CONTRACT NUMBER: CA92577 (NCI)
EY12599 (NEI)

GM23652 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Jan 8) 99 (1) 178-83. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020416
Entered Medline: 20020415

AB Pathological angiogenesis contributes directly to profound loss of vision associated with many diseases of the eye. Recent work suggests that human tyrosyl- and **tryptophanyl**-tRNA synthetases (TrpRS) link protein synthesis to signal transduction pathways including angiogenesis. In this study, we show that a recombinant form of a COOH-terminal fragment of TrpRS is a potent antagonist of vascular endothelial growth factor-induced angiogenesis in a mouse model and of naturally occurring retinal angiogenesis in the neonatal mouse. The angiostatic activity is dose-dependent in both systems. The recombinant fragment is similar in size to one generated naturally by alternative splicing and can be produced by proteolysis of the full-length protein. In contrast, the full-length protein is inactive as an antagonist of angiogenesis. These results suggest that fragments of TrpRS, as naturally occurring and potentially nonimmunogenic anti-angiogenics, can be used for the treatment of neovascular eye diseases.

L6 ANSWER 2 OF 6 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002056933 MEDLINE
DOCUMENT NUMBER: 21642696 PubMed ID: 11773626
TITLE: A human aminoacyl-tRNA synthetase as a regulator of angiogenesis.
AUTHOR: **Wakasugi Keisuke**; Slike Bonnie M; Hood John; Otani Atsushi; Ewalt Karla L; Friedlander Martin; Cheresh David A; **Schimmel Paul**
CORPORATE SOURCE: The Skaggs Institute for Chemical Biology and Department of Molecular Biology, The Scripps Research Institute, La Jolla, CA 92037, USA.
CONTRACT NUMBER: CA92577 (NCI)
EY12599 (NEI)
GM23562 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Jan 8) 99 (1) 173-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020416
Entered Medline: 20020415

AB Aminoacyl-tRNA synthetases catalyze the first step of protein synthesis. It was shown recently that human tyrosyl-tRNA synthetase (TyrRS) can be split into two fragments having distinct cytokine activities, thereby linking protein synthesis to cytokine signaling pathways. **Tryptophanyl**-tRNA synthetase (TrpRS) is a close homologue of

TyrRS. A natural fragment, herein designated as mini TrpRS, was shown by others to be produced by alternative splicing. Production of this fragment is reported to be stimulated by IFN-gamma, a cytokine that also stimulates production of angiostatic factors. Mini TrpRS is shown here to be angiostatic in a mammalian cell culture system, the chicken embryo, and two independent angiogenesis assays in the mouse. The full-length enzyme is inactive in the same assays. Thus, protein synthesis may be linked to the regulation of angiogenesis by a natural fragment of TrpRS.

L6 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:287264 BIOSIS
DOCUMENT NUMBER: PREV200100287264
TITLE: Truncated fragments of aminoacyl-tRNA synthetases are potent angiostatic agents for retinal angiogenesis.
AUTHOR(S): Otani, A. (1); Slike, B. (1); Ewalt, K. (1); **Schimmel, P. (1)**; Friedlander, M. (1)
CORPORATE SOURCE: (1) Depts. of Cell Biology and Molecular Biology, Scripps Res Inst, La Jolla, CA, 92037 USA
SOURCE: IOVS, (March 15, 2001) Vol. 42, No. 4, pp. S93. print. Meeting Info.: Annual Meeting of the Association for Research in Vision and Ophthalmology Fort Lauderdale, Florida, USA April 29-May 04, 2001
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L6 ANSWER 4 OF 6 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 96133898 MEDLINE
DOCUMENT NUMBER: 96133898 PubMed ID: 8552597
TITLE: Evidence that two present-day components needed for the genetic code appeared after nucleated cells separated from eubacteria.
AUTHOR: Ribas de Pouplana L; Frugier M; Quinn C L; **Schimmel P**
CORPORATE SOURCE: Department of Biology, Massachusetts Institute of Technology, Cambridge 02139, USA.
CONTRACT NUMBER: GM 23562 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1996 Jan 9) 93 (1) 166-70. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-U40714
ENTRY MONTH: 199602
ENTRY DATE: Entered STN: 19960306
Last Updated on STN: 19980206
Entered Medline: 19960222

AB The trinucleotide/amino acid relationships of the present-day genetic code are established by the amino-acylation reactions of tRNA synthetases, whereby each of 20 specific amino acids is attached to its cognate tRNAs, which bear anticodon trinucleotides. Because of its universality, the appearance of the modern genetic code is thought to predate the separation of prokaryotic and eukaryotic organisms in the universal phylogenetic tree. In the light of new sequence information, we present here a phylogenetic analysis that shows an unusual picture for tyrosyl- and

tryptophanyl-tRNA synthetases. Ij particular, the eukaryotic tyrosyl- and **tryptophanyl**-tRNA synthetases are more related to each other than to their respective prokaryotic counterparts. In contrast, each of the other 18 eukaryotic synthetases is more related to its prokaryotic counterpart than to any eukaryotic synthetase specific for a different amino acid. Our results raise the possibility that present day tyrosyl- and **tryptophanyl**-tRNA synthetases appeared after the separation of nucleated cells from eubacteria. The results have implications for the development of the genetic code.

L6 ANSWER 5 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1985:63893 BIOSIS
DOCUMENT NUMBER: BR28:63893
TITLE: SIZE POLYMORPHISM AND THE STRUCTURE OF AMINOACYL TRANSFER RNA SYNTHETASES.
AUTHOR(S): **SCHIMMEL P**; JASIN M; REGAN L
CORPORATE SOURCE: DEP. BIOL., MASSACHUSETTS INST. TECHNOL., CAMBRIDGE, MASS. 02139.
SOURCE: MINISYMPOSIUM ON AMINOACYL-TRNA SYNTHETASES: STRUCTURE-FUNCTION, REGULATION, AND TRNA RECOGNITION HELD AT THE 74TH ANNUAL MEETING OF THE AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, SAN FRANCISCO, CALIF., USA, JUNE 6, 1983. FED PROC, (1984) 43 (15), 2987-2990.
CODEN: FEPRA7. ISSN: 0014-9446.
FILE SEGMENT: BR; OLD
LANGUAGE: English

L6 ANSWER 6 OF 6 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 1979:90906 BIOSIS
DOCUMENT NUMBER: BR17:30906
TITLE: THE BINDING OF **TRYPTOPHANYL** TRANSFER RNA SYNTHETASE TO TYROSYL TRANSFER RNA IN ESCHERICHIA-COLI.
AUTHOR(S): FAYERMAN J T; DYSON H J; VISWANATHAN T S; BUDZIK G P; **SCHIMMEL P R**
SOURCE: Abstr. Annu. Meet. Am. Soc. Microbiol., (1979) (79), 152.
CODEN: ASMACK. ISSN: 0094-8519.
DOCUMENT TYPE: Conference
FILE SEGMENT: BR; OLD
LANGUAGE: Unavailable

=> d his

(FILE 'HOME' ENTERED AT 10:22:26 ON 24 OCT 2002)

FILE 'MEDLINE, CANCERLIT, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 10:22:58 ON 24 OCT 2002
L1 1460 S (SCHIMMEL-P? OR WAKASUGI-K?)/AU
L2 730 S L1 AND TRNA
L3 644 S L2 AND SYNTHETASE
L4 1 S L3 AND ROSSMANN
L5 17 S L1 AND TRYPTOPHANYL?
L6 6 DUP REM L5 (11 DUPLICATES REMOVED)

=> s Rossmann
L7 600 ROSSMANN

=> s l7 and tryptophanyl? or trpRS
L8 177 L7 AND TRYPTOPHANYL? OR TRPRS

=> s l8 and (fragment or truncat? or cleavage)
L9 19 L8 AND (FRAGMENT OR TRUNCAT? OR CLEAVAGE)

=> dup rem l9
PROCESSING COMPLETED FOR L9
L10 6 DUP REM L9 (13 DUPLICATES REMOVED)

=> d ibib abs 1-6

L10 ANSWER 1 OF 6 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002056934 MEDLINE
DOCUMENT NUMBER: 21642695 PubMed ID: 11773625
TITLE: A **fragment** of human **TrpRS** as a potent antagonist of ocular angiogenesis.
AUTHOR: Otani Atsushi; Slike Bonnie M; Dorrell Michael I; Hood John; Kinder Karen; Ewalt Karla L; Cheresh David; Schimmel Paul; Friedlander Martin
CORPORATE SOURCE: Department of Cell Biology, The Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA 92037, USA.
CONTRACT NUMBER: CA92577 (NCI)
EY12599 (NEI)
GM23652 (NIGMS)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Jan 8) 99 (1) 178-83. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200204
ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020416
Entered Medline: 20020415
AB Pathological angiogenesis contributes directly to profound loss of vision associated with many diseases of the eye. Recent work suggests that human tyrosyl- and tryptophanyl-tRNA synthetases (**TrpRS**) link protein synthesis to signal transduction pathways including angiogenesis. In this study, we show that a recombinant form of a COOH-terminal **fragment** of **TrpRS** is a potent antagonist of vascular endothelial growth factor-induced angiogenesis in a mouse model and of naturally occurring retinal angiogenesis in the neonatal mouse. The angiostatic activity is dose-dependent in both systems. The recombinant **fragment** is similar in size to one generated naturally by alternative splicing and can be produced by proteolysis of the full-length protein. In contrast, the full-length protein is inactive as an antagonist of angiogenesis. These results suggest that **fragments** of **TrpRS**, as naturally occurring and potentially nonimmunogenic anti-angiogenics, can be used for the treatment of neovascular eye diseases.

L10 ANSWER 2 OF 6 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002056933 MEDLINE
DOCUMENT NUMBER: 21642696 PubMed ID: 11773626
TITLE: A human aminoacyl-tRNA synthetase as a regulator of angiogenesis.
AUTHOR: Wakasugi Keisuke; Slike Bonnie M; Hood John; Otani Atsushi;

Ewalt Karla L; Friedlander Martin; Cheresh David A; Schimmel Paul

CORPORATE SOURCE: The Skaggs Institute for Chemical Biology and Department of Molecular Biology, The Scripps Research Institute, La Jolla, CA 92037, USA.

CONTRACT NUMBER: CA92577 (NCI)
EY12599 (NEI)
GM23562 (NIGMS)

SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2002 Jan 8) 99 (1) 173-7.
Journal code: 7505876. ISSN: 0027-8424.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200204

ENTRY DATE: Entered STN: 20020125
Last Updated on STN: 20020416
Entered Medline: 20020415

AB Aminoacyl-tRNA synthetases catalyze the first step of protein synthesis. It was shown recently that human tyrosyl-tRNA synthetase (TyrRS) can be split into two **fragments** having distinct cytokine activities, thereby linking protein synthesis to cytokine signaling pathways. Tryptophanyl-tRNA synthetase (**TrpRS**) is a close homologue of TyrRS. A natural **fragment**, herein designated as mini **TrpRS**, was shown by others to be produced by alternative splicing. Production of this **fragment** is reported to be stimulated by IFN-gamma, a cytokine that also stimulates production of angiostatic factors. Mini **TrpRS** is shown here to be angiostatic in a mammalian cell culture system, the chicken embryo, and two independent angiogenesis assays in the mouse. The full-length enzyme is inactive in the same assays. Thus, protein synthesis may be linked to the regulation of angiogenesis by a natural **fragment** of **TrpRS**.

L10 ANSWER 3 OF 6 MEDLINE DUPLICATE 3

ACCESSION NUMBER: 2000178918 MEDLINE

DOCUMENT NUMBER: 20178918 PubMed ID: 10716174

TITLE: 2.9 A crystal structure of ligand-free tryptophanyl-tRNA synthetase: domain movements **fragment** the adenine nucleotide binding site.

AUTHOR: Ilyin V A; Temple B; Hu M; Li G; Yin Y; Vachette P; Carter C W Jr

CORPORATE SOURCE: Department of Biochemistry and Biophysics, University of North Carolina, Chapel Hill 27514, USA.

CONTRACT NUMBER: GM48519 (NIGMS)

SOURCE: PROTEIN SCIENCE, (2000 Feb) 9 (2) 218-31.
Journal code: 9211750. ISSN: 0961-8368.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: PDB-1D2R

ENTRY MONTH: 200004

ENTRY DATE: Entered STN: 20000505
Last Updated on STN: 20000505
Entered Medline: 20000421

AB The crystal structure of ligand-free tryptophanyl-tRNA synthetase (**TrpRS**) was solved at 2.9 A using a combination of molecular replacement and maximum-entropy map/phase improvement. The dimeric structure (R = 23.7, Rfree = 26.2) is asymmetric, unlike that of the

TrpRS tryptophanyl-5'AMP complex (TAM; Doublie S, Bricogne G, Gilmore CJ, Carter CW Jr, 1995, Structure 3:17-31). In agreement with small-angle solution X-ray scattering experiments, unliganded **TrpRS** has a conformation in which both monomers open, leaving only the tryptophan-binding regions of their active sites intact. The amino terminal alphaA-helix, TIGN, and KMSKS signature sequences, and the distal helical domain rotate as a single rigid body away from the dinucleotide-binding fold domain, opening the AMP binding site, seen in the TAM complex, into two halves. Comparison of side-chain packing in ligand-free **TrpRS** and the TAM complex, using identification of nonpolar nuclei (Ilyin VA, 1994, Protein Eng 7:1189-1195), shows that significant repacking occurs between three relatively stable core regions, one of which acts as a bearing between the other two. These domain rearrangements provide a new structural paradigm that is consistent in detail with the "induced-fit" mechanism proposed for TyrRS by Fersht et al. (Fersht AR, Knill-Jones JW, Beduelle H, Winter G, 1988, Biochemistry 27:1581-1587). Coupling of ATP binding determinants associated with the two catalytic signature sequences to the helical domain containing the presumptive anticodon-binding site provides a mechanism to coordinate active-site chemistry with relocation of the major tRNA binding determinants.

L10 ANSWER 4 OF 6 MEDLINE
ACCESSION NUMBER: 94220246 MEDLINE
DOCUMENT NUMBER: 94220246 PubMed ID: 8166950
TITLE: Overcoming non-isomorphism by phase permutation and likelihood scoring: solution of the **TrpRS** crystal structure.
AUTHOR: Doublie S; Xiang S; Gilmore C J; Bricogne G; Carter C W Jr
CORPORATE SOURCE: Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill 27599-7260.
CONTRACT NUMBER: 26203
SOURCE: ACTA CRYSTALLOGRAPHICA. SECTION A, FOUNDATIONS OF CRYSTALLOGRAPHY, (1994 Mar 1) 50 (Pt 2) 164-82. Journal code: 8305825. ISSN: 0108-7673.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199405
ENTRY DATE: Entered STN: 19940613
Last Updated on STN: 19980206
Entered Medline: 19940527

AB Entropy maximization to maximum likelihood, constrained jointly by the best available experimental phases and by a sufficiently good envelope, can bring about substantial model-independent map improvement, even at medium (3.1 A) resolution [Xiang, Carter, Bricogne & Gilmore (1993). Acta Cryst. D49, 193-212]. In the crystal structure determination of the Bacillus stearothermophilus tryptophanyl-tRNA synthetase (**TrpRS**), however, the following had to be dealt with simultaneously: (1) a serious lack of isomorphism in the heavy-atom derivatives, resulting in large starting-phase errors; and (2) an initially poorly known molecular envelope. Because the constraints--both phases and envelope--were insufficiently well determined at the outset, maximum-entropy solvent flattening as previously applied was unsuccessful. Rather than improving the maps, it led to a deterioration of their quality, accompanied by a dramatic decrease of the log-likelihood gain as phases were extended from about 5 A resolution to the 2.9 A limit of the diffraction data. This deadlock was broken by the identification of strong reflections, which

were initially unphased and which were inaccessible by maximum-entropy extrapolation from the phased ones, and by permutation of the phases of these reflections so as to sample the space of possible electron-density and envelope modifications they represented. Permutation was carried out by successive full and incomplete factorial designs [Carter & Carter (1979). J. Biol. Chem. 254, 12219-12223] for 28 strong reflections selected in decreasing order of their 'renormalized' structure-factor amplitudes. The permuted reflections included one reflection for which the probability distribution from multiple isomorphous replacement with anomalous scattering (MIRAS) indicated an incorrect phase with a high figure of merit and which consequently had a large renormalized structure factor. A similar permutation was carried out for six different binary choices related to the calculation and description of the molecular envelope. Permutation experiments were scored using the log-likelihood gain and contrasts for each main effect were analyzed by multiple-regression least squares. Student t tests provided significant and reliable indications for a large majority of the permuted reflections and for all six hypotheses related to the molecular envelope. The resulting phase improvement made it possible to assign positions (hitherto unobtainable) for nine of the ten selenium atoms in an isomorphous difference Fourier map for selenomethionine-substituted **TrpRS** crystals and hence to solve the structure. Phase-permutation methods continued to be useful in producing improved maps from all the available isomorphous-replacement phase information and therefore played a critical role in solving the structure.(ABSTRACT **TRUNCATED** AT 400 WORDS)

L10 ANSWER 5 OF 6 MEDLINE
ACCESSION NUMBER: 93185665 MEDLINE
DOCUMENT NUMBER: 93185665 PubMed ID: 8444184
TITLE: Are the tryptophanyl-tRNA synthetase and the peptide-chain-release factor from higher eukaryotes one and the same protein?.
AUTHOR: Frolova LYu; Fleckner J; Justesen J; Timms K M; Tate W P; Kisselev L L; Haenni A L
CORPORATE SOURCE: Institut Jacques Monod, Paris, France.
SOURCE: EUROPEAN JOURNAL OF BIOCHEMISTRY, (1993 Mar 1) 212 (2) 457-66.
Journal code: 0107600. ISSN: 0014-2956.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199304
ENTRY DATE: Entered STN: 19930416
Last Updated on STN: 19980206
Entered Medline: 19930408

AB Recently, cDNA clones encoding the bovine (b) [M. Garret, B. Pajot, V. Trezeguet, J. Labouesse, M. Merle, J.-C. Gandar, J.-P. Benedetto, M.-L. Sallafranque, J. Alterio, M. Gueguen, C. Sarger, B. Labouesse and J. Bonnet (1991) Biochemistry 30, 7809-7817] and human (h) [L. Yu. Frolova, M. A. Sudomoina, A. Yu. Grigorieva, O. L. Zinovieva and L. L. Kisselev (1991) Gene 109, 291-296] tryptophanyl-tRNA synthetases (**TrpRS**) were sequenced; the deduced amino acid sequences exhibit typical structural features of class I aminoacyl-tRNA synthetases [G. Eriani, M. Delarue, O. Poch, J. Gangloff and D. Moras (1990) Nature 237, 203-206] and limited, although significant, similarity with bacterial **TrpRS**. Independently, it was shown that a major protein whose synthesis is

stimulated in human cell cultures by interferon gamma [J. Fleckner, H. H. Rasmussen and J. Justesen (1991) Proc. Natl Acad. Sci. USA 88, 11,520-11,524], and interferons gamma or alpha [B. Y. Rubins, S. L. Anderson, L. Xing, R. J. Powell and W. P. Tate (1991) J. Biol. Chem. 226, 24,245-24,248], exhibits **TrpRS** activity and an amino acid sequence identical to that of hTrpRS. The amino acid sequences of bTrpRS and hTrpRS are highly similar and are surprisingly very similar to the amino acid sequence deduced from a cloned and sequenced cDNA reported to encode rabbit (r) peptide-chain-release factor (RF) [C. C. Lee, W. J. Craigen, D. M. Muzny, E. Harlow and C. T. Caskey (1990) Proc. Natl Acad. Sci. USA 87, 3508-3512]. This close similarity between mammalian **TrpRS** and cloned RF is unexpected given the distinct functional properties of these proteins. Consequently, the question arises as to whether the mammalian **TrpRS** and RF activities reside on identical or very similar polypeptides. Alternatively, one may assume that the cloned rabbit cDNA encodes a protein other than rRF. Several properties (immunochemical, biochemical and physico-chemical) of mammalian **TrpRS** and RF have been compared. rTrpRS and rRF have distinct thermostability behaviours, and dissimilar chromatographic profiles on phosphocellulose. Both the anti-bTrpRS polyclonal antibodies and the monoclonal antibody Am2 strongly inhibit the bTrpRS and hTrpRS aminoacylation activities, but not the rRF activity. In addition, neither bTrpRS nor hTrpRS exhibit RF activity.(ABSTRACT **TRUNCATED** AT 400 WORDS)

L10 ANSWER 6 OF 6 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 89211991 MEDLINE
DOCUMENT NUMBER: 89211991 PubMed ID: 3149612
TITLE: Cloning and nucleotide sequence of the structural gene coding for Bacillus subtilis tryptophanyl-tRNA synthetase.
AUTHOR: Chow K C; Wong J T
CORPORATE SOURCE: Department of Biochemistry, University of Toronto, Ont., Canada.
SOURCE: GENE, (1988 Dec 20) 73 (2) 537-43.
Journal code: 7706761. ISSN: 0378-1119.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M24068
ENTRY MONTH: 198906
ENTRY DATE: Entered STN: 19900306
Last Updated on STN: 19980206
Entered Medline: 19890605

AB A 1.47-kb DNA **fragment** that carries the tryptophanyl-tRNA synthetase (**TrpRS**) gene of Bacillus subtilis has been cloned into the pUC8 plasmid. The recombinant plasmid, pTSQ2, conferred temperature-resistance to the temperature-sensitive trpS ts mutant of B. subtilis through chromosomal transformation, and to that of Escherichia coli through complementation. The pTSQ2 could be stably maintained in E. coli DH5 alpha, causing in the host cell a 200-fold amplification of **TrpRS** activity. The complete nucleotide sequence of the cloned **fragment** has been determined. A putative transcriptional promoter, a Shine-Dalgarno sequence, the 990-bp trpS gene proper, as well as a transcriptional terminator have been identified.

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FILE 'MEDLINE, CANCERLIT, BIOSIS, EMBASE, SCISEARCH' ENTERED AT 10:22:58 ON 24 OCT 2002

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L1          1460 S (SCHIMMEL-P? OR WAKASUGI-K?)/AU
L2           730 S L1 AND TRNA
L3           644 S L2 AND SYNTHETASE
L4             1 S L3 AND ROSSMANN
L5            17 S L1 AND TRYPTOPHANYL?
L6             6 DUP REM L5 (11 DUPLICATES REMOVED)
L7           600 S ROSSMANN
L8           177 S L7 AND TRYPTOPHANYL? OR TRPRS
L9            19 S L8 AND (FRAGMENT OR TRUNCAT? OR CLEAVAGE)
L10            6 DUP REM L9 (13 DUPLICATES REMOVED)

=> s "Rossmann fold"
L11         399 "ROSSMANN FOLD"

=> s l11 and (TRYPTOPHANYL? OR TRPRS)
L12           4 L11 AND (TRYPTOPHANYL? OR TRPRS)

=> dup rem l12
PROCESSING COMPLETED FOR L12
L13           1 DUP REM L12 (3 DUPLICATES REMOVED)

=> d ibib abs l13

L13  ANSWER 1 OF 1     MEDLINE                              DUPLICATE 1
ACCESSION NUMBER:    96134815     MEDLINE
DOCUMENT NUMBER:     96134815   PubMed ID: 8555191
TITLE:               Escherichia coli tryptophanyl-tRNA synthetase
                     mutants selected for tryptophan auxotrophy implicate the
                     dimer interface in optimizing amino acid binding.
AUTHOR:              Sever S; Rogers K; Rogers M J; Carter C Jr; Soll D
CORPORATE SOURCE:    Department of Molecular Biophysics and Biochemistry, Yale
                     University, New Haven, Connecticut 06520-8114, USA.
SOURCE:              BIOCHEMISTRY, (1996 Jan 9) 35 (1) 32-40.
                     Journal code: 0370623. ISSN: 0006-2960.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
OTHER SOURCE:        GENBANK-U38647
ENTRY MONTH:         199602
ENTRY DATE:          Entered STN: 19960312
                     Last Updated on STN: 19980206
                     Entered Medline: 19960227
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AB Tryptophan auxotrophs of Escherichia coli in which mutations were mapped to the trpS locus (encoding **tryptophanyl**-tRNA synthetase) have been previously isolated. We have investigated the **tryptophanyl**-tRNA synthetase (**TrpRS**) purified from six auxotrophic strains for changes in amino acid activation and aminoacylation. Steady-state kinetic analyses show that these mutant **TrpRS** proteins have increases in the apparent KM for tryptophan, decreases in turnover number, or both, without significant changes in the apparent KM for ATP or tRNA(Trp). The crystal structure of a highly homologous **tryptophanyl**-tRNA synthetase from Bacillus stearothermophilus in a complex with the cognate aminoacyl adenylate allowed us to place the mutations in a structural context. The mutations in the enzymes are

located in the KMSKS loop (M196I), in or near the active site (D112E, P129S, A133E) or far from the active site. The last three mutants (T60R, L91F, G329S) could not be predicted by examination of the protein structure as they line an interface between the C-terminal alpha-helix of one subunit and the **Rossmann folds** of both subunits, thus affecting a specific region of the dimer interface. These results support a role for dimerization in properly configuring the two active sites of the dimeric enzymes in the Trp/Tyr subclass of class I aminoacyl-tRNA synthetases in order to achieve optimal catalysis.

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 NEWS  4  Apr 09  ZDB will be removed from STN
 NEWS  5  Apr 19  US Patent Applications available in IFICDB, IFIPAT, and
IFIUDB
 NEWS  6  Apr 22  Records from IP.com available in CAPLUS, HCAPLUS, and
ZCAPLUS
 NEWS  7  Apr 22  BIOSIS Gene Names now available in TOXCENTER
 NEWS  8  Apr 22  Federal Research in Progress (FEDRIP) now available
 NEWS  9  Jun 03  New e-mail delivery for search results now available
 NEWS 10  Jun 10  MEDLINE Reload
 NEWS 11  Jun 10  PCTFULL has been reloaded
 NEWS 12  Jul 02  FOREGE no longer contains STANDARDS file segment
 NEWS 13  Jul 22  USAN to be reloaded July 28, 2002;
                  saved answer sets no longer valid
 NEWS 14  Jul 29  Enhanced polymer searching in REGISTRY
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 NEWS 17  Aug 08  PHARMAMarketLetter(PHARMAML) - new on STN
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                  now available on STN
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 NEWS 23  Sep 03  JAPIO has been reloaded and enhanced
 NEWS 24  Sep 16  Experimental properties added to the REGISTRY file
 NEWS 25  Sep 16  Indexing added to some pre-1967 records in CA/CAPLUS
 NEWS 26  Sep 16  CA Section Thesaurus available in CAPLUS and CA
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 NEWS 28  Oct 21  EVENTLINE has been reloaded

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